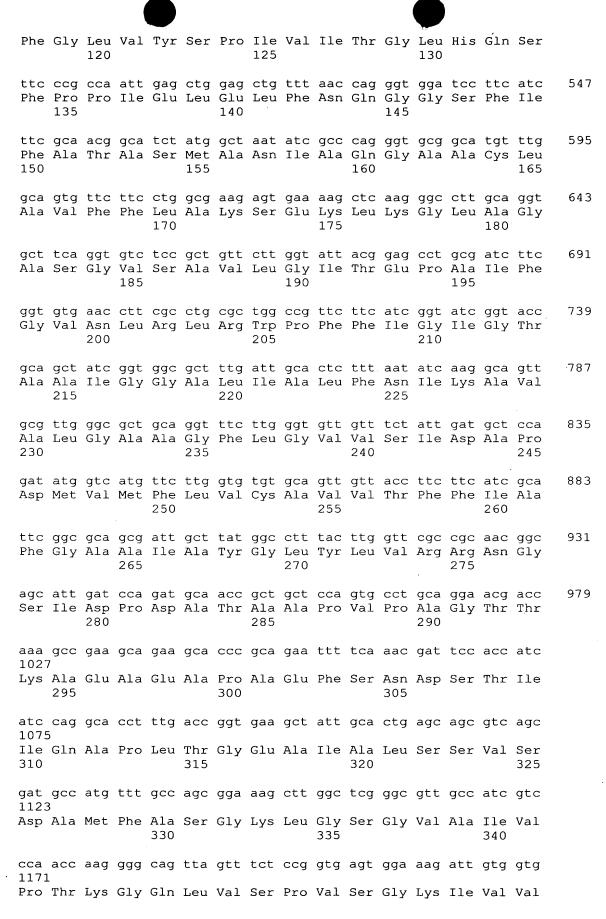
## SEQUENCE LISTING

| <110         | K<br>S<br>Z                                      | Pompejus, Markus<br>Kroger, Burkhard<br>Schroder, Hartwig<br>Zelder, Oskar  |      |       |      |      |      |       |       |      |     |      |       |            |        |     |
|--------------|--|---|------|-------|------|------|------|-------|-------|------|-----|------|-------|------------|--------|-----|
| <120         | O> C<br>P  | Haberhauer, Gregor CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PHOSPHOENOLPYRUVATE:SUGAR PHOSPHOTRANSFERASE SYSTEM PROTEINS BGI-122CP  34 |      |       |      |      |      |       |       |      |     |      |       |            |        |     |
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| <213<br><213 | 2> D   | 1<br>1527<br>DNA<br>Corynebacterium glutamicum  |      |       |      |      |      |       |       |      |     |      |       |            |        |     |
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|              |  | ttg<br>Leu  |      |       |      |      |      |       |       |      |     |      |       |            |        | 163 |
|              |  | cca<br>Pro  |      |       |      |      |      |       |       |      |     |      |       |            |        | 211 |
|              | _  | ggc<br>Gly<br>40  |      |       |      |      |      | _     |       | _    |     |      |       | -          | -      | 259 |
|              |  | gag<br>Glu  |      |       |      |      |      |       |       |      |     |      |       |            |        | 307 |
|              |  | act<br>Thr  |      |       |      |      |      |       |       |      |     |      |       |            |        | 355 |
|              |  | att<br>Ile  |      |       |      | _    |      |       |       |      | -   | _    | _     |            |        | 403 |
|              |  | cag<br>Gln  |      |       |      |      |      |       |       |      |     |      |       |            |        | 451 |
| ttc          | ggt  | ctg   | gtc  | tac   | tca  | cca  | atc  | gtc   | atc   | act  | ggt | ctq  | cac   | cag        | tcc    | 499 |



345 355 350 gca ttc cca tct ggc cat gct ttc gca gtt cgc acc aag gct gag gat Ala Phe Pro Ser Gly His Ala Phe Ala Val Arg Thr Lys Ala Glu Asp ggt too aat gtg gat ato ttg atg cac att ggt tto gac aca gta aac 1267 Gly Ser Asn Val Asp Ile Leu Met His Ile Gly Phe Asp Thr Val Asn 375 380 ctc aac ggc acg cac ttt aac ccg ctg aag aag cag ggc gat gaa gtc 1315 Leu Asn Gly Thr His Phe Asn Pro Leu Lys Lys Gln Gly Asp Glu Val 390 395 aaa gca ggg gag ctg ctg tgt gaa ttc gat att gat gcc att aag gct 1363 Lys Ala Gly Glu Leu Leu Cys Glu Phe Asp Ile Asp Ala Ile Lys Ala 410 415 420 gca ggt tat gag gta acc acg ccg att gtt gtt tcg aat tac aag aaa 1411 Ala Gly Tyr Glu Val Thr Thr Pro Ile Val Val Ser Asn Tyr Lys Lys 425 430 acc qga cct qta aac act tac qqt ttq qqc qaa att qaa qcq qqa qcc 1459 Thr Gly Pro Val Asn Thr Tyr Gly Leu Gly Glu Ile Glu Ala Gly Ala 440 445 aac ctg ctc aac gtc gca aag aaa gaa gcg gtg cca gca aca cca 1504 Asn Leu Leu Asn Val Ala Lys Lys Glu Ala Val Pro Ala Thr Pro taagttgaaa ccttgagtgt tcg 1527

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Ser Trp Ile Leu Ala Thr Ile Glu Lys Phe Leu His Lys Arg Leu Lys 50 55 60

Gly Thr Ala Asp Phe Leu Ile Thr Pro Val Leu Thr Leu Leu Leu Thr 65 70 75 80

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Gln Gly Asp Glu Val Lys Ala Gly Glu Leu Leu Cys Glu Phe Asp Ile 405 Asp Ala Ile Lys Ala Ala Gly Tyr Glu Val Thr Thr Pro Ile Val Val 420 Ser Asn Tyr Lys Lys Thr Gly Pro Val Asn Thr Tyr Gly Leu Gly Glu Ile Glu Ala Gly Ala Asn Leu Leu Asn Val Ala Lys Lys Glu Ala Val Pro Ala Thr Pro 465 <210> 3 <211> 1109 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(1086) <223> FRXA00315 <400> 3 48 tat gat ttc ggc ggt cca gtc ggc ggt ctg ctc ttc ggt ctg gtc tac Tyr Asp Phe Gly Gly Pro Val Gly Gly Leu Phe Gly Leu Val Tyr tca cca atc gtc atc act ggt ctg cac cag tcc ttc ccg cca att gag 96 Ser Pro Ile Val Ile Thr Gly Leu His Gln Ser Phe Pro Pro Ile Glu 25 ctg gag ctg ttt aac cag ggt gga tcc ttc atc ttc gca acg gca tct 144 Leu Glu Leu Phe Asn Gln Gly Gly Ser Phe Ile Phe Ala Thr Ala Ser atg gct aat atc gcc cag ggt gcg gca tgt ttg gca gtg ttc ttc ctq 192 Met Ala Asn Ile Ala Gln Gly Ala Ala Cys Leu Ala Val Phe Phe Leu gcg aag agt gaa aag ctc aag ggc ctt gca ggt gct tca ggt gtc tcc 240 Ala Lys Ser Glu Lys Leu Lys Gly Leu Ala Gly Ala Ser Gly Val Ser gct gtt ctt ggt att acg gag cct gcg atc ttc ggt gtg aac ctt cgc 288 Ala Val Leu Gly Ile Thr Glu Pro Ala Ile Phe Gly Val Asn Leu Arg 85 ctg cgc tgg ccg ttc ttc atc ggt atc ggt acc gca gct atc ggt ggc 336 Leu Arg Trp Pro Phe Phe Ile Gly Ile Gly Thr Ala Ala Ile Gly Gly 100 105 110 gct ttg att gca ctc ttt aat atc aag gca gtt gcg ttg ggc gct gca 384 Ala Leu Ile Ala Leu Phe Asn Ile Lys Ala Val Ala Leu Gly Ala Ala 115 120 ggt ttc ttg ggt gtt gtt tct att gat gct cca gat atg gtc atg ttc 432

Gly Phe Leu Gly Val Val Ser Ile Asp Ala Pro Asp Met Val Met Phe

130 135 140 ttg gtg tgt gca gtt gtt acc ttc ttc atc gca ttc ggc gca gcg att 480 Leu Val Cys Ala Val Val Thr Phe Phe Ile Ala Phe Gly Ala Ala Ile 145 150 155 528 gct tat ggc ctt tac ttg gtt cgc cgc aac ggc agc att gat cca gat Ala Tyr Gly Leu Tyr Leu Val Arg Arg Asn Gly Ser Ile Asp Pro Asp 170 165 576 gca acc gct gct cca gtg cct gca gga acg acc aaa gcc gaa gca gaa Ala Thr Ala Ala Pro Val Pro Ala Gly Thr Thr Lys Ala Glu Ala Glu 180 185 gca ccc gca gaa ttt tca aac gat tcc acc atc atc cag gca cct ttg 624 Ala Pro Ala Glu Phe Ser Asn Asp Ser Thr Ile Ile Gln Ala Pro Leu 200 acc ggt gaa gct att gca ctg agc agc gtc agc gat gcc atg ttt gcc 672 Thr Gly Glu Ala Ile Ala Leu Ser Ser Val Ser Asp Ala Met Phe Ala 210 215 age gga aag ett gge teg gge gtt gee ate gte eea aee aag ggg eag 720 Ser Gly Lys Leu Gly Ser Gly Val Ala Ile Val Pro Thr Lys Gly Gln 225 230 235 tta gtt tct ccg gtg agt gga aag att gtg gtg gca ttc cca tct ggc 768 Leu Val Ser Pro Val Ser Gly Lys Ile Val Val Ala Phe Pro Ser Gly 250 255 245 cat gct ttc gca gtt cgc acc aag gct gag gat ggt tcc aat gtg gat 816 His Ala Phe Ala Val Arg Thr Lys Ala Glu Asp Gly Ser Asn Val Asp 260 265 ate ttg atg cac att ggt ttc gac aca gta aac ctc aac ggc acg cac 864 Ile Leu Met His Ile Gly Phe Asp Thr Val Asn Leu Asn Gly Thr His 275 280 ttt aac ccg ctg aag aag cag ggc gat gaa gtc aaa gca ggg gag ctg 912 Phe Asn Pro Leu Lys Lys Gln Gly Asp Glu Val Lys Ala Gly Glu Leu 290 295 300 ctg tgt gaa ttc gat att gat gcc att aag gct gca ggt tat gag gta 960 Leu Cys Glu Phe Asp Ile Asp Ala Ile Lys Ala Ala Gly Tyr Glu Val 305 310 315 acc acg ccg att gtt gtt tcg aat tac aag aaa acc gga cct gta aac Thr Thr Pro Ile Val Val Ser Asn Tyr Lys Lys Thr Gly Pro Val Asn 325 330 act tac ggt ttg ggc gaa att gaa gcg gga gcc aac ctg ctc aac gtc 1056 Thr Tyr Gly Leu Gly Glu Ile Glu Ala Gly Ala Asn Leu Leu Asn Val 345 gca aag aaa gaa gcg gtg cca gca aca cca taagttgaaa ccttgagtgt Ala Lys Lys Glu Ala Val Pro Ala Thr Pro 355 360

tcg 1109

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<211> 362

<212> PRT

<213> Corynebacterium glutamicum

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Leu Glu Leu Phe Asn Gln Gly Gly Ser Phe Ile Phe Ala Thr Ala Ser 35 40 45

Met Ala Asn Ile Ala Gln Gly Ala Ala Cys Leu Ala Val Phe Phe Leu 50 55 60

Ala Lys Ser Glu Lys Leu Lys Gly Leu Ala Gly Ala Ser Gly Val Ser 65 70 75 80

Ala Val Leu Gly Ile Thr Glu Pro Ala Ile Phe Gly Val Asn Leu Arg 85 90 95

Leu Arg Trp Pro Phe Phe Ile Gly Ile Gly Thr Ala Ala Ile Gly Gly 100 105 110

Ala Leu Ile Ala Leu Phe Asn Ile Lys Ala Val Ala Leu Gly Ala Ala 115 120 125

Gly Phe Leu Gly Val Val Ser Ile Asp Ala Pro Asp Met Val Met Phe 130 135 140

Leu Val Cys Ala Val Val Thr Phe Phe Ile Ala Phe Gly Ala Ala Ile 145 150 155 160

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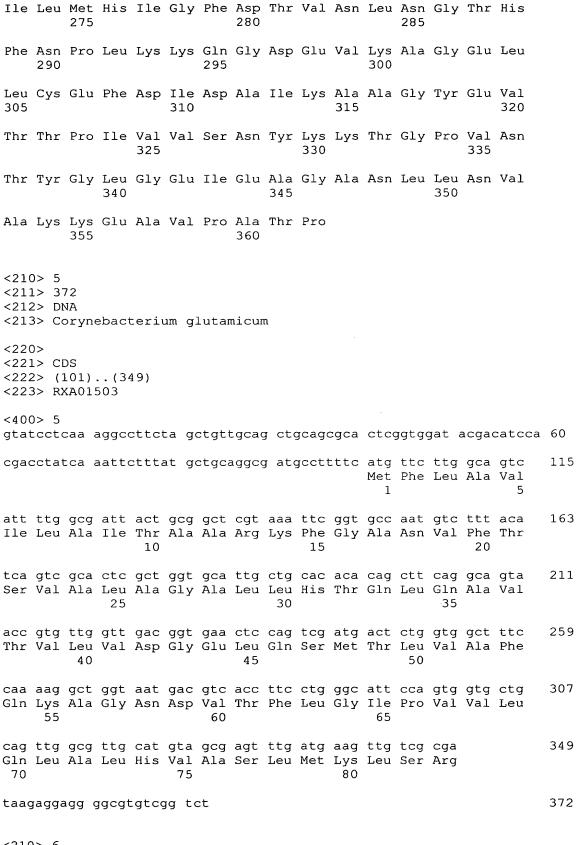
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Thr Gly Glu Ala Ile Ala Leu Ser Ser Val Ser Asp Ala Met Phe Ala 210 215 220

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Gln Leu Gln Ala Val Thr Val Leu Val Asp Gly Glu Leu Gln Ser Met 35 40 45

Thr Leu Val Ala Phe Gln Lys Ala Gly Asn Asp Val Thr Phe Leu Gly 50 55 60

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Leu Ser Arg

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<211> 2187

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXN01299

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aat tcc tcg ctt gtc cgg ctg gat gtc gat ttc ggc gac tcc acc acg  $\phantom{0}$  163 Asn Ser Ser Leu Val Arg Leu Asp Val Asp Phe Gly Asp Ser Thr Thr  $\phantom{0}$  10  $\phantom{0}$  15  $\phantom{0}$  20

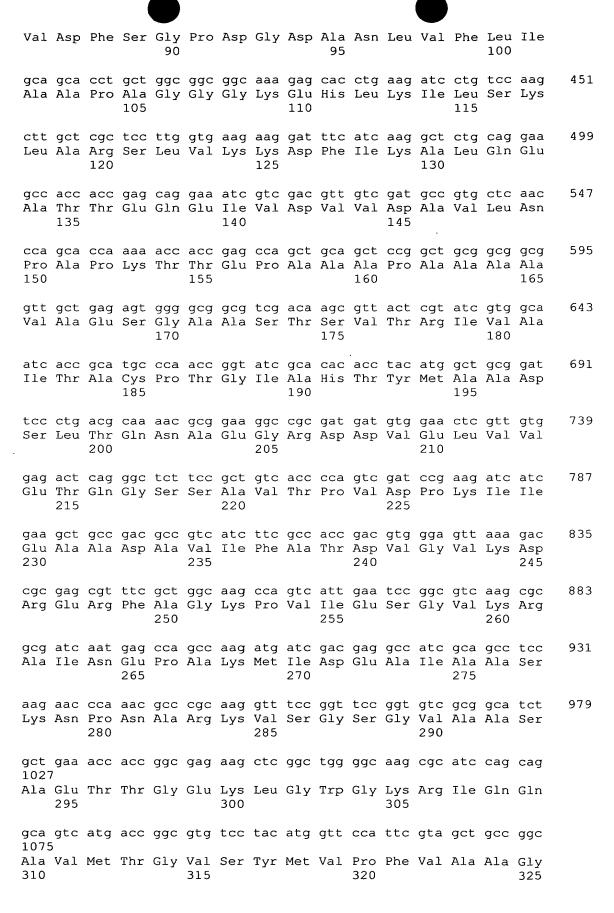
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tcc ggc acc ggc gtt cct ggt caa gtt gct atc ccc cac tgc cgt tcc 307 Ser Gly Thr Gly Val Pro Gly Gln Val Ala Ile Pro His Cys Arg Ser 55 60 65

gaa gcc gta tct gtc cct acc ttg ggc ttt gct cgc ctg agc aag ggt 355 Glu Ala Val Ser Val Pro Thr Leu Gly Phe Ala Arg Leu Ser Lys Gly 70 75 80 85

gtg gac ttc agc gga cct gat ggc gat gcc aac ttg gtg ttc ctc att 403



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685

<212> PRT

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Asp Arg Glu Ala Lys Ser Gly Thr Gly Val Pro Gly Gln Val Ala Ile 50 55 60

Pro His Cys Arg Ser Glu Ala Val Ser Val Pro Thr Leu Gly Phe Ala 65 70 75 80

Arg Leu Ser Lys Gly Val Asp Phe Ser Gly Pro Asp Gly Asp Ala Asn 85 . 90 95

Leu Val Phe Leu Ile Ala Ala Pro Ala Gly Gly Lys Glu His Leu
100 105 110

Lys Ile Leu Ser Lys Leu Ala Arg Ser Leu Val Lys Lys Asp Phe Ile 115 120 125

Lys Ala Leu Gln Glu Ala Thr Thr Glu Gln Glu Ile Val Asp Val Val 130 135 140

Asp Ala Val Leu Asn Pro Ala Pro Lys Thr Thr Glu Pro Ala Ala Ala 145 150 155 160

Pro Ala Ala Ala Val Ala Glu Ser Gly Ala Ala Ser Thr Ser Val 165 170 175

Thr Arg Ile Val Ala Ile Thr Ala Cys Pro Thr Gly Ile Ala His Thr 180 185 190

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Val Glu Leu Val Val Glu Thr Gln Gly Ser Ser Ala Val Thr Pro Val 210 215 220

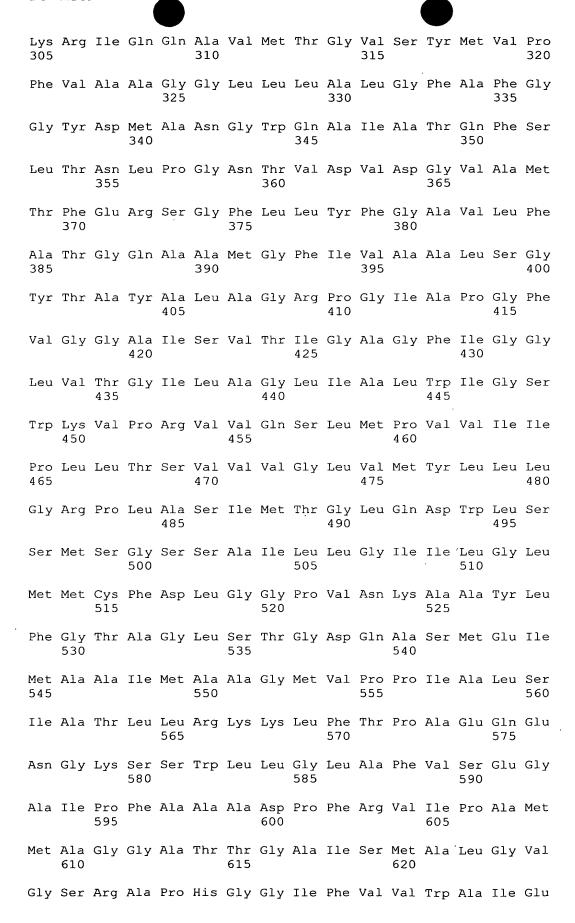
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Val Gly Val Lys Asp Arg Glu Arg Phe Ala Gly Lys Pro Val Ile Glu 245 250 255

Ser Gly Val Lys Arg Ala Ile Asn Glu Pro Ala Lys Met Ile Asp Glu 260 265 270

Ala Ile Ala Ala Ser Lys Asn Pro Asn Ala Arg Lys Val Ser Gly Ser 275 280 285

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625 630 635 640

Pro Trp Trp Gly Trp Leu Ile Ala Leu Ala Ala Gly Thr Ile Val Ser 655

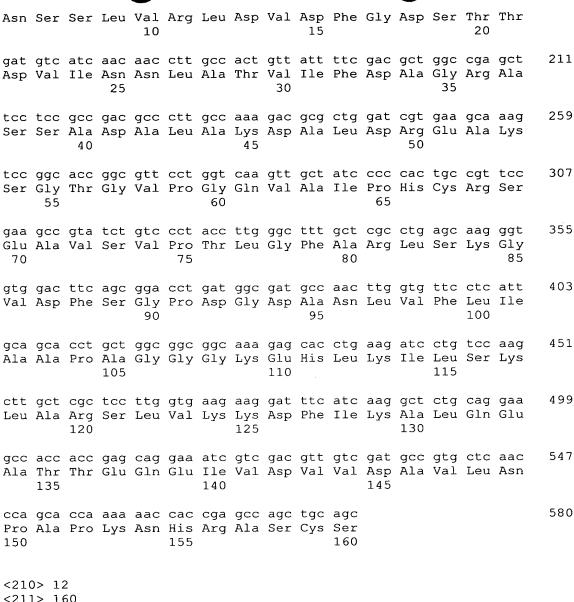
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680

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464 gta aac gca taatcggacc ttgacccgat gtc Val Asn Ala 145 <210> 10 <211> 147 <212> PRT <213> Corynebacterium glutamicum Met Glu Ile Met Ala Ala Ile Met Ala Ala Gly Met Val Pro Pro Ile Ala Leu Ser Ile Ala Thr Leu Leu Arg Lys Lys Leu Phe Thr Pro Ala 20 25 Glu Glu Asn Gly Lys Ser Ser Trp Leu Leu Gly Leu Ala Phe Val Ser Glu Gly Ala Ile Pro Phe Ala Ala Asp Pro Phe Arg Val Ile 50 Pro Ala Met Met Ala Gly Gly Ala Thr Thr Gly Ala Ile Ser Met Ala Leu Gly Val Gly Ser Arg Ala Pro His Gly Gly Ile Phe Val Val Trp Ala Ile Glu Pro Trp Trp Gly Trp Leu Ile Ala Leu Ala Ala Gly Thr 100 105 Ile Val Ser Thr Ile Val Val Ile Ala Leu Lys Gln Phe Trp Pro Asn 115 120 125 Lys Ala Val Ala Ala Glu Val Ala Lys Gln Glu Ala Gln Gln Ala Ala 130 135 140 Val Asn Ala 145 <210> 11 <211> 580 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(580) <223> FRXA01883 <400> 11 cgactgcggc gtctcttcct ggcactacca ttcctcgtcc tgaccaactc gccacagctg 60 gtgcaacggt cacccaagtc aaaggattga aagaatcagc atg aat agc gta aat 115 Met Asn Ser Val Asn 1 aat tee teg ett gte egg etg gat gte gat tte gge gae tee ace acg 163



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<212> PRT

<213> Corynebacterium glutamicum

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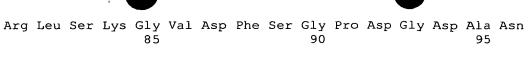
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Asp Arg Glu Ala Lys Ser Gly Thr Gly Val Pro Gly Gln Val Ala Ile

Pro His Cys Arg Ser Glu Ala Val Ser Val Pro Thr Leu Gly Phe Ala



Leu Val Phe Leu Ile Ala Ala Pro Ala Gly Gly Gly Lys Glu His Leu 100 105 110

Lys Ile Leu Ser Lys Leu Ala Arg Ser Leu Val Lys Lys Asp Phe Ile 115 120 125

Lys Ala Leu Gln Glu Ala Thr Thr Glu Gln Glu Ile Val Asp Val Val 130 135 140

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<223> FRXA01889

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Thr Tyr Met Ala Ala Asp Ser Leu Thr Gln Asn Ala Glu Gly Arg Asp
15 20 25.

gat gtg gaa ctc gtt gtg gag act cag ggc tct tcc gct gtc acc cca 208 Asp Val Glu Leu Val Val Glu Thr Gln Gly Ser Ser Ala Val Thr Pro 30 35 40

gtc gat ccg aag atc atc gaa gct gcc gac gcc gtc atc ttc gcc acc 256
Val Asp Pro Lys Ile Ile Glu Ala Ala Asp Ala Val Ile Phe Ala Thr
45 50 55 60

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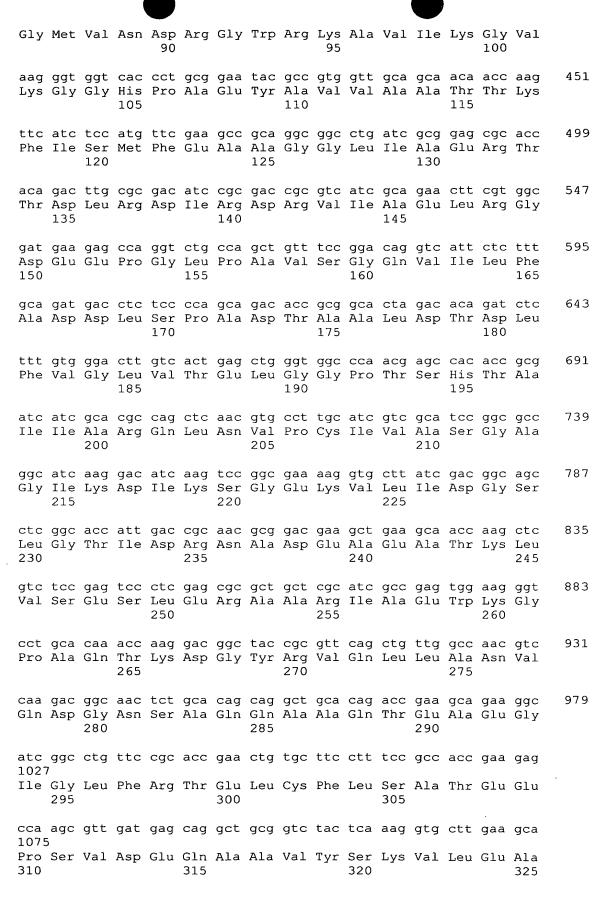
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Ser Gly Val Ala Ala Ser Ala Glu Thr Thr Gly Glu Lys Leu Gly Trp 115 ggc aag cgc atc cag cag gca gtc atg acc ggc gtg tcc tac atg gtt 496 Gly Lys Arg Ile Gln Gln Ala Val Met Thr Gly Val Ser Tyr Met Val 130 135 cca ttc gta gct gcc ggc ggc ctc ctg ttg gct ctc ggc ttc gca ttc 544 Pro Phe Val Ala Ala Gly Gly Leu Leu Leu Ala Leu Gly Phe Ala Phe 150 ggt gga tac gac atg gcg aac ggc tgg caa gca atc gcc acc cag ttc 592 Gly Gly Tyr Asp Met Ala Asn Gly Trp Gln Ala Ile Ala Thr Gln Phe 160 165 tct ctg acc aac ctg cca ggc aac acc gtc gat gtt gac 631 Ser Leu Thr Asn Leu Pro Gly Asn Thr Val Asp Val Asp 180 <210> 14 <211> 185 <212> PRT <213> Corynebacterium glutamicum <400> 14 Val Ala Ile Thr Ala Cys Pro Thr Gly Ile Ala His Thr Tyr Met Ala Ala Asp Ser Leu Thr Gln Asn Ala Glu Gly Arg Asp Asp Val Glu Leu 20 Val Val Glu Thr Gln Gly Ser Ser Ala Val Thr Pro Val Asp Pro Lys Ile Ile Glu Ala Ala Asp Ala Val Ile Phe Ala Thr Asp Val Gly Val Lys Asp Arg Glu Arg Phe Ala Gly Lys Pro Val Ile Glu Ser Gly Val Lys Arg Ala Ile Asn Glu Pro Ala Lys Met Ile Asp Glu Ala Ile Ala Ala Ser Lys Asn Pro Asn Ala Arg Lys Val Ser Gly Ser Gly Val Ala Ala Ser Ala Glu Thr Thr Gly Glu Lys Leu Gly Trp Gly Lys Arg Ile Gln Gln Ala Val Met Thr Gly Val Ser Tyr Met Val Pro Phe Val Ala 135 Ala Gly Gly Leu Leu Ala Leu Gly Phe Ala Phe Gly Gly Tyr Asp Met Ala Asn Gly Trp Gln Ala Ile Ala Thr Gln Phe Ser Leu Thr Asn 170 Leu Pro Gly Asn Thr Val Asp Val Asp

| <211<br><212 | )> 15<br>L> 41<br>2> DN<br>3> Co | 16<br>1A          | ebact     | eriu     | ım g] | Lutan | nicum             | n         |           |     |     |     |           |           |     |     |
|--------------|----------------------------------|-------------------|-----------|----------|-------|-------|-------------------|-----------|-----------|-----|-----|-----|-----------|-----------|-----|-----|
| <222         | L> CI<br>2> (1                   | OS<br>L)<br>KAOOS |           | ı        |       |       |                   |           |           |     |     |     |           |           |     |     |
| <400         | )> 15                            | 5                 |           |          |       |       |                   |           |           |     |     |     |           |           |     |     |
|              |                                  |                   |           |          |       |       | gca<br>Ala        |           |           |     |     |     |           |           |     | 48  |
|              |                                  |                   |           |          |       |       | aca<br>Thr        |           |           |     |     |     |           |           |     | 96  |
|              |                                  |                   |           |          |       |       | aag<br>Lys<br>40  |           |           |     |     |     |           |           |     | 144 |
|              |                                  |                   |           |          |       |       | aaa<br>Lys        |           |           |     |     |     |           |           |     | 192 |
|              |                                  |                   |           |          |       |       | atg<br>Met        |           |           |     |     |     |           |           |     | 240 |
|              |                                  |                   |           |          |       |       | gaa<br>Glu        |           |           |     |     |     |           |           |     | 288 |
|              |                                  |                   |           |          |       |       | gat<br>Asp        |           |           |     |     |     |           |           |     | 336 |
|              |                                  |                   |           |          |       |       | gaa<br>Glu<br>120 |           |           |     |     |     |           |           |     | 384 |
|              | gac<br>Asp<br>130                | _                 | taad      | ctact    | ett a | aaaa  | ggaco             | ga aa     | aa        |     |     |     |           |           |     | 416 |
| <211<br><212 | 0> 16<br>L> 13<br>2> PF<br>3> Co | 31<br>RT          | ebact     | ceriu    | ım gl | Lutan | nicum             | n         |           |     |     |     |           |           |     |     |
| <400         | )> 16                            | 5                 |           |          |       |       |                   |           |           |     |     |     |           |           |     |     |
|              |                                  |                   | Ile       | Leu<br>5 | Glu   | Lys   | Ala               | Ala       | Ala<br>10 | Pro | Ala | Lys | Gln       | Lys<br>15 | Ala |     |
| Pro          | Ala                              | Val               | Ala<br>20 | Pro      | Ala   | Val   | Thr               | Pro<br>25 | Thr       | Asp | Ala | Pro | Ala<br>30 | Ala       | Ser |     |

Val Gln Ser Lys Thr His Asp Lys Ile Leu Thr Val Cys Gly Asn Gly 40 Leu Gly Thr Ser Leu Phe Leu Lys Asn Thr Leu Glu Gln Val Phe Asp Thr Trp Gly Trp Gly Pro Tyr Met Thr Val Glu Ala Thr Asp Thr Ile 75 Ser Ala Lys Gly Lys Ala Lys Glu Ala Asp Leu Ile Met Thr Ser Gly Glu Ile Ala Arg Thr Leu Gly Asp Val Gly Ile Pro Val His Val Ile 100 Asn Asp Phe Thr Ser Thr Asp Glu Ile Asp Ala Ala Leu Arg Glu Arg 120 Tyr Asp Ile 130 <210> 17 <211> 1827 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1804) <223> RXN01244 <400> 17 gatatgtgtt tgtttgtcaa tatccaaatg tttgaatagt tgcacaactg ttggttttgt 60 ggtgatcttg aggaaattaa ctcaatgatt gtgaggatgg gtg gct act gtg gct 115 Val Ala Thr Val Ala 1 gat gtg aat caa gac act gta ctg aag ggc acc ggc gtt gtc ggt gga 163 Asp Val Asn Gln Asp Thr Val Leu Lys Gly Thr Gly Val Val Gly Gly 10 20 gtc cgt tat gca agc gcg gtg tgg att acc cca cgc ccc gaa cta ccc 211 Val Arg Tyr Ala Ser Ala Val Trp Ile Thr Pro Arg Pro Glu Leu Pro 25 35 caa gca ggc gaa gtc gtc gcc gaa gaa aac cgt gaa gca gag cag gag 259 Gln Ala Gly Glu Val Val Ala Glu Glu Asn Arg Glu Ala Glu Gln Glu 40 307 cgt ttc gac gcc gct gca gcc aca gtc tct tct cgt ttg ctt gag cgc Arg Phe Asp Ala Ala Ala Thr Val Ser Ser Arg Leu Leu Glu Arg 55 60 355 tee gaa get get gaa gga eea get gag gtg ett aaa get aet get Ser Glu Ala Ala Glu Gly Pro Ala Ala Glu Val Leu Lys Ala Thr Ala 75 403 ggc atg gtc aat gac cgt ggc tgg cgt aag gct gtc atc aag ggt gtc



ttc cca gag tcc aag gtc gtt gtc cgc tcc ctc gac gca ggt tct gac Phe Pro Glu Ser Lys Val Val Val Arg Ser Leu Asp Ala Gly Ser Asp aag cca gtt cca ttc gca tcg atg gct gat gag atg aac cca gca ctg 1171 Lys Pro Val Pro Phe Ala Ser Met Ala Asp Glu Met Asn Pro Ala Leu 350 345 ggt gtt cgt ggc ctg cgt atc gca cgt gga cag gtt gat ctg ctg act 1219 Gly Val Arg Gly Leu Arg Ile Ala Arg Gly Gln Val Asp Leu Leu Thr 365 360 cgc cag ctc gac gca att gcg aag gcc agc gaa gaa ctc ggc cgt ggc 1267 Arg Gln Leu Asp Ala Ile Ala Lys Ala Ser Glu Glu Leu Gly Arg Gly 385 375 380 gac gac gcc cca acc tgg gtt atg gct cca atg gtg gct acc gct tat 1315 Asp Asp Ala Pro Thr Trp Val Met Ala Pro Met Val Ala Thr Ala Tyr 390 395 400 gaa gca aag tgg ttt gct gac atg tgc cgt gag cgt ggc cta atc gcc 1363 Glu Ala Lys Trp Phe Ala Asp Met Cys Arg Glu Arg Gly Leu Ile Ala 420 410 415 ggc gcc atg atc gaa gtt cca gca gca tcc ctg atg gca gac aag atc 1411 Gly Ala Met Ile Glu Val Pro Ala Ala Ser Leu Met Ala Asp Lys Ile 425 430 atg cet cae etg gae ttt gtt tee ate ggt ace aac gae etg ace cag 1459 Met Pro His Leu Asp Phe Val Ser Ile Gly Thr Asn Asp Leu Thr Gln 440 445 450 tac acc atg gca gcg gac cgc atg tct cct gag ctt gcc tac ctg acc 1507 Tyr Thr Met Ala Ala Asp Arg Met Ser Pro Glu Leu Ala Tyr Leu Thr 460 455 gat cct tgg cag cca gca gtc ctg cgc ctg atc aag cac acc tgt gac 1555 Asp Pro Trp Gln Pro Ala Val Leu Arg Leu Ile Lys His Thr Cys Asp 470 485 gaa ggt gct cgc ttt aac acc ccg gtc ggt gtt tgt ggt gaa gca gca Glu Gly Ala Arg Phe Asn Thr Pro Val Gly Val Cys Gly Glu Ala Ala 490 495 gca gac cca ctg ttg gca act gtc ctc acc ggt ctt ggc gtg aac tcc 1651 Ala Asp Pro Leu Leu Ala Thr Val Leu Thr Gly Leu Gly Val Asn Ser 505

ctg tee gea gea tee act get ete gea gea gte ggt gea aag etg tea 1699

Leu Ser Ala Ala Ser Thr Ala Leu Ala Ala Val Gly Ala Lys Leu Ser 520 530

gag gtc acc ctg gaa acc tgt aag aag gca gca gca gca ctt gac 1747

Glu Val Thr Leu Glu Thr Cys Lys Lys Ala Ala Glu Ala Ala Leu Asp 535 540 545

gct gaa ggt gca act gaa gca cgc gat gct gta cgc gca gtg atc gac 1795

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Glu Ala Glu Glu Arg Phe Asp Ala Ala Ala Ala Thr Val Ser Ser 50 60

Arg Leu Leu Glu Arg Ser Glu Ala Ala Glu Gly Pro Ala Ala Glu Val 65 70 75 80

Leu Lys Ala Thr Ala Gly Met Val Asn Asp Arg Gly Trp Arg Lys Ala 85 90 95

Val Ile Lys Gly Val Lys Gly Gly His Pro Ala Glu Tyr Ala Val Val 100 105 110

Ala Ala Thr Thr Lys Phe Ile Ser Met Phe Glu Ala Ala Gly Gly Leu 115 120 125

Ile Ala Glu Arg Thr Thr Asp Leu Arg Asp Ile Arg Asp Arg Val Ile 130 135 140

Ala Glu Leu Arg Gly Asp Glu Glu Pro Gly Leu Pro Ala Val Ser Gly 145 150 155 160

Gln Val Ile Leu Phe Ala Asp Asp Leu Ser Pro Ala Asp Thr Ala Ala 165 170 175

Leu Asp Thr Asp Leu Phe Val Gly Leu Val Thr Glu Leu Gly Gly Pro

180 185 190 Thr Ser His Thr Ala Ile Ile Ala Arg Gln Leu Asn Val Pro Cys Ile 200 Val Ala Ser Gly Ala Gly Ile Lys Asp Ile Lys Ser Gly Glu Lys Val Leu Ile Asp Gly Ser Leu Gly Thr Ile Asp Arg Asn Ala Asp Glu Ala Glu Ala Thr Lys Leu Val Ser Glu Ser Leu Glu Arg Ala Ala Arg Ile Ala Glu Trp Lys Gly Pro Ala Gln Thr Lys Asp Gly Tyr Arg Val Gln Leu Leu Ala Asn Val Gln Asp Gly Asn Ser Ala Gln Gln Ala Ala Gln 280 Thr Glu Ala Glu Gly Ile Gly Leu Phe Arg Thr Glu Leu Cys Phe Leu Ser Ala Thr Glu Glu Pro Ser Val Asp Glu Gln Ala Ala Val Tyr Ser 305 310 Lys Val Leu Glu Ala Phe Pro Glu Ser Lys Val Val Arg Ser Leu 325 330 Asp Ala Gly Ser Asp Lys Pro Val Pro Phe Ala Ser Met Ala Asp Glu 340 350 Met Asn Pro Ala Leu Gly Val Arg Gly Leu Arg Ile Ala Arg Gly Gln Val Asp Leu Leu Thr Arg Gln Leu Asp Ala Ile Ala Lys Ala Ser Glu 370 375 380 Glu Leu Gly Arg Gly Asp Asp Ala Pro Thr Trp Val Met Ala Pro Met 390 395 Val Ala Thr Ala Tyr Glu Ala Lys Trp Phe Ala Asp Met Cys Arg Glu 410 Arg Gly Leu Ile Ala Gly Ala Met Ile Glu Val Pro Ala Ala Ser Leu Met Ala Asp Lys Ile Met Pro His Leu Asp Phe Val Ser Ile Gly Thr Asn Asp Leu Thr Gln Tyr Thr Met Ala Ala Asp Arg Met Ser Pro Glu Leu Ala Tyr Leu Thr Asp Pro Trp Gln Pro Ala Val Leu Arg Leu Ile Lys His Thr Cys Asp Glu Gly Ala Arg Phe Asn Thr Pro Val Gly Val 490 Cys Gly Glu Ala Ala Ala Asp Pro Leu Leu Ala Thr Val Leu Thr Gly

505

Leu Gly Val Asn Ser Leu Ser Ala Ala Ser Thr Ala Leu Ala Ala Val 515 520 525

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gct gct gaa gga cca gct gag gtg ctt aaa gct act gct ggc atg  $\,$  163 Ala Ala Glu Gly Pro Ala Ala Glu Val Leu Lys Ala Thr Ala Gly Met  $\,$  10  $\,$  15  $\,$  20

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gac ctc tcc cca gca gac acc gcg gca cta gac aca gat ctc ttt gtg 451 Asp Leu Ser Pro Ala Asp Thr Ala Ala Leu Asp Thr Asp Leu Phe Val 105 110 115

gga ctt gtc act gag ctg ggt ggc cca acg agc cac acc gcg atc atc 499 Gly Leu Val Thr Glu Leu Gly Gly Pro Thr Ser His Thr Ala Ile Ile

gca cgc cag ctc aac gtg cct tgc atc gtc gca tcc ggc gcc ggc atc Ala Arg Gln Leu Asn Val Pro Cys Ile Val Ala Ser Gly Ala Gly Ile aaq qac atc aaq tcc qqc qaa aaq qtq ctt atc qac qqc aqc ctc qqc Lys Asp Ile Lys Ser Gly Glu Lys Val Leu Ile Asp Gly Ser Leu Gly acc att gac ege aac geg gac gaa get gaa gea aec aag ete gte tee Thr Ile Asp Arg Asn Ala Asp Glu Ala Glu Ala Thr Lys Leu Val Ser gag tcc ctc gag cgc gct gct cgc atc gcc gag tgg aag ggt cct gca Glu Ser Leu Glu Arg Ala Ala Arg Ile Ala Glu Trp Lys Gly Pro Ala caa acc aag gac ggc tac cgc gtt cag ctg ttg gcc aac gtc caa gac Gln Thr Lys Asp Gly Tyr Arg Val Gln Leu Leu Ala Asn Val Gln Asp ggc aac tot gca cag cag gct gca cag acc gaa gca gaa ggc atc ggc Gly Asn Ser Ala Gln Gln Ala Ala Gln Thr Glu Ala Glu Gly Ile Gly ctg ttc cgc acc gaa ctg tgc ttc ctt tcc gcc acc gaa gag cca agc Leu Phe Arg Thr Glu Leu Cys Phe Leu Ser Ala Thr Glu Glu Pro Ser gtt gat gag cag gct gcg gtc tac tca aag gtg ctt gaa gca ttc cca Val Asp Glu Gln Ala Ala Val Tyr Ser Lys Val Leu Glu Ala Phe Pro gag tee aag gte gtt gte ege tee ete gae gea ggt tet gae aag eea Glu Ser Lys Val Val Val Arg Ser Leu Asp Ala Gly Ser Asp Lys Pro gtt cca ttc gca tcg atg gct gat gag atg aac cca gca ctg ggt gtt Val Pro Phe Ala Ser Met Ala Asp Glu Met Asn Pro Ala Leu Gly Val cgt ggc ctg cgt atc gca cgt gga cag gtt gat ctg ctg act cgc cag Arg Gly Leu Arg Ile Ala Arg Gly Gln Val Asp Leu Leu Thr Arg Gln ctc qac gca att qcq aaq qcc agc gaa gaa ctc ggc cqt ggc gac gac Leu Asp Ala Ile Ala Lys Ala Ser Glu Glu Leu Gly Arg Gly Asp Asp qcc cca acc tqq qtt atq qct cca atq qtq qct acc qct tat qaa qca Ala Pro Thr Trp Val Met Ala Pro Met Val Ala Thr Ala Tyr Glu Ala aag tgg ttt gct gac atg tgc cgt gag cgt ggc cta atc gcc ggc gcc Lys Trp Phe Ala Asp Met Cys Arg Glu Arg Gly Leu Ile Ala Gly Ala 

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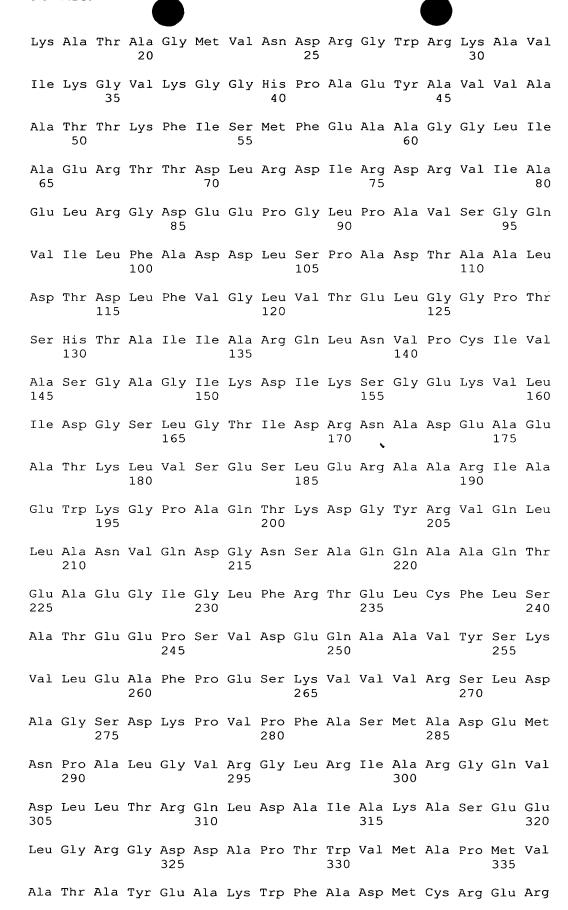
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|          |            | 340 |     |     |            |            | 345 |     |     |            |            | 350 |     |     |  |
| Gly Leu  | Ile<br>355 | Ala | Gly | Ala | Met        | Ile<br>360 | Glu | Val | Pro | Ala        | Ala<br>365 | Ser | Leu | Met |  |
| Ala Asp  | _          | Ile | Met | Pro | His<br>375 | Leu        | Asp | Phe | Val | Ser<br>380 | Ile        | Gly | Thr | Asn |  |

Asp Leu Thr Gln Tyr Thr Met Ala Ala Asp Arg Met Ser Pro Glu Leu 385 390 395 400

Ala Tyr Leu Thr Asp Pro Trp Gln Pro Ala Val Leu Arg Leu Ile Lys 405 410 415

His Thr Cys Asp Glu Gly Ala Arg Phe Asn Thr Pro Val Gly Val Cys 420 425 430

Gly Glu Ala Ala Asp Pro Leu Leu Ala Thr Val Leu Thr Gly Leu 435 440 445

Gly Val Asn Ser Leu Ser Ala Ala Ser Thr Ala Leu Ala Ala Val Gly 450 455 460

Ala Lys Leu Ser Glu Val Thr Leu Glu Thr Cys Lys Lys Ala Ala Glu 465 470 475 480

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gta acc gtc ggt tcc tcc gtt ggc ctg cac gca cgt cca gca tcc atc 163 Val Thr Val Gly Ser Ser Val Gly Leu His Ala Arg Pro Ala Ser Ile 10 15 20

atc gct gaa gcg gct gct gag tac gac gac gaa atc ttg ctg acc ctg 211
Ile Ala Glu Ala Ala Glu Tyr Asp Asp Glu Ile Leu Leu Thr Leu
25 30 35

gtt ggc tcc gat gat gac gaa gag acc gac gcg tcc tct tcc ctc atg 259 Val Gly Ser Asp Asp Asp Glu Glu Thr Asp Ala Ser Ser Ser Leu Met 40 45 50



Trp Arg Glu Gly Ile Arg Ala Ala Gly Val Leu Leu Glu Lys Thr Asn age att gat tee gee tae ace gat gee atg ate gee age gtg gaa gaa 259 Ser Ile Asp Ser Ala Tyr Thr Asp Ala Met Ile Ala Ser Val Glu Glu 307 aaa qqc ccc tac att qtq qtc qct cca qqt ttc qct ttc qcg cac gcc Lys Gly Pro Tyr Ile Val Val Ala Pro Gly Phe Ala Phe Ala His Ala 355 cgc ccc agc aga gca gtc cgc gag acc gct atg tcg tgg gtg cgc ctg Arg Pro Ser Arg Ala Val Arg Glu Thr Ala Met Ser Trp Val Arg Leu gcc tcc cct gtt tcc ttc ggt cac agt aag aat gat ccc ctc aat ctc 403 Ala Ser Pro Val Ser Phe Gly His Ser Lys Asn Asp Pro Leu Asn Leu ate gtt gct ctc gct gcc aaa gat gcc acc gca cat acc caa gcg atg 451 Ile Val Ala Leu Ala Ala Lys Asp Ala Thr Ala His Thr Gln Ala Met 110 gcg gca ttg gct aaa gct tta gga aaa tac cga aag gat ctc gac gag 499 Ala Ala Leu Ala Lys Ala Leu Gly Lys Tyr Arg Lys Asp Leu Asp Glu 130 120 125 508 gca caa agt Ala Gln Ser 135 <210> 24 <211> 136 <212> PRT <213> Corynebacterium glutamicum <400> 24 Met Phe Val Leu Lys Asp Leu Leu Lys Ala Glu Arg Ile Glu Leu Asp Arg Thr Val Thr Asp Trp Arg Glu Gly Ile Arg Ala Ala Gly Val Leu 30 20 Leu Glu Lys Thr Asn Ser Ile Asp Ser Ala Tyr Thr Asp Ala Met Ile Ala Ser Val Glu Glu Lys Gly Pro Tyr Ile Val Val Ala Pro Gly Phe 50 Ala Phe Ala His Ala Arg Pro Ser Arg Ala Val Arg Glu Thr Ala Met Ser Trp Val Arg Leu Ala Ser Pro Val Ser Phe Gly His Ser Lys Asn Asp Pro Leu Asn Leu Ile Val Ala Leu Ala Ala Lys Asp Ala Thr Ala His Thr Gln Ala Met Ala Ala Leu Ala Lys Ala Leu Gly Lys Tyr Arg 120

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ggt gtc cgc acc att ctt ggt gaa ctg gtc ccc gca ttc caa ggt att 148 Gly Val Arg Thr Ile Leu Gly Glu Leu Val Pro Ala Phe Gln Gly Ile 30 45

gct gcg aag gtt gtt ccc gga gct atc ccc gca ttg gat gca ccg atc 196 Ala Ala Lys Val Val Pro Gly Ala Ile Pro Ala Leu Asp Ala Pro Ile 50 55 60

gtg ttc ccc tac gcg cag aac gcc gtt ctc att ggt ttc ttg tct tcc 244 Val Phe Pro Tyr Ala Gln Asn Ala Val Leu Ile Gly Phe Leu Ser Ser 65 70 75

ttc gtc ggt ggc ttg gtt ggc ctg act gtt ctt gca tcg tgg ctg aac 292 Phe Val Gly Gly Leu Val Gly Leu Thr Val Leu Ala Ser Trp Leu Asn 80 85 90

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Pro Ala Phe Gly Val Ala Leu Ile Leu Pro Gly Leu Val Pro His Phe
95 100 105

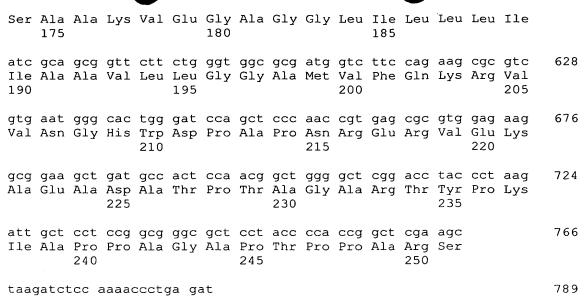
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ctc cct gct ttc ctg ctt ggt gtg ctt ggt tcc ttc ggg tca gag aac 484 Leu Pro Ala Phe Leu Leu Gly Val Leu Gly Ser Phe Gly Ser Glu Asn 145

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Thr Thr Phe Gly Asp Ala Asp Phe Gly Trp Phe Gly Ile Val Val Gly
160 165 170

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- 34 -

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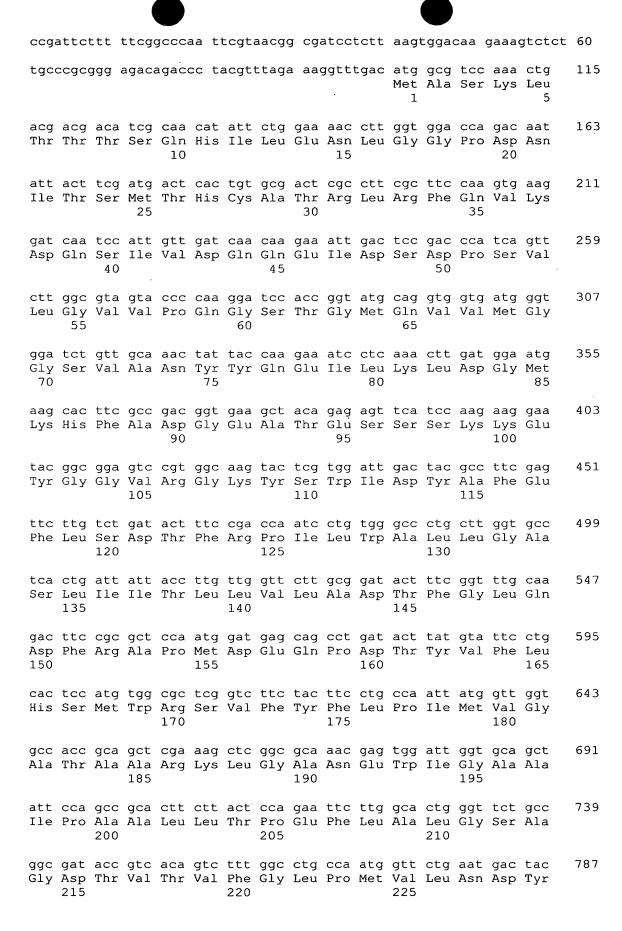
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Trp Leu Met Ile Leu Gly Phe Ala Ile Ser Leu Val Leu Ala Arg Phe

110

105

acc aac ctg cgt tat gtc ttg ctc aac gga cac cac gtg ctg ttg atg 499 Thr Asn Leu Arg Tyr Val Leu Leu Asn Gly His His Val Leu Leu Met 120 125 tgc acc atg ctc acc atg gtc ttg gcc acc gga aga gtt gat gcg tgg 547 Cys Thr Met Leu Thr Met Val Leu Ala Thr Gly Arg Val Asp Ala Trp 135 140 atc ttc 553 Ile Phe 150 <210> 28 <211> 151 <212> PRT <213> Corynebacterium glutamicum <400> 28 Met Asp Trp Leu Thr Ile Pro Leu Phe Leu Val Asn Glu Ile Leu Ala 5 Val Pro Ala Phe Leu Ile Gly Ile Ile Thr Ala Val Gly Leu Gly Ala Met Gly Arg Ser Val Gly Gln Val Ile Gly Gly Ala Ile Lys Ala Thr 35 Leu Gly Phe Leu Leu Ile Gly Ala Gly Ala Thr Leu Val Thr Ala Ser Leu Glu Pro Leu Gly Ala Met Ile Met Gly Ala Thr Gly Met Arg Gly 70 65 Val Val Pro Thr Asn Glu Ala Ile Ala Gly Ile Ala Gln Ala Glu Tyr Gly Ala Gln Val Ala Trp Leu Met Ile Leu Gly Phe Ala Ile Ser Leu 100 105 110 Val Leu Ala Arg Phe Thr Asn Leu Arg Tyr Val Leu Leu Asn Gly His 115 120 His Val Leu Leu Met Cys Thr Met Leu Thr Met Val Leu Ala Thr Gly 130 140 135 Arg Val Asp Ala Trp Ile Phe 145 150 <210> 29 <211> 2172 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(2149) <223> RXN01943 <400> 29



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atg gac cca tgg ttg ggc tac acc att ggt atc gca gtt gca ttc ttc 1459 Met Asp Pro Trp Leu Gly Tyr Thr Ile Gly Ile Ala Val Ala Phe Phe 440 445 gtt tcc atg ttc ctt gtt ctc gca ctg gac tac cgt tcc aac gaa gag 1507 Val Ser Met Phe Leu Val Leu Ala Leu Asp Tyr Arg Ser Asn Glu Glu cgc gat gag gca cgt gca aag gtt gct gcc aag cag gca gaa gaa Arg Asp Glu Ala Arg Ala Lys Val Ala Ala Asp Lys Gln Ala Glu Glu 470 475 485 gat ctg aag gca gaa gct aat gca act cct gca gct cca gta gct gct 1603 Asp Leu Lys Ala Glu Ala Asn Ala Thr Pro Ala Ala Pro Val Ala Ala 490 495 gca ggt gcg gga gcc ggt gca ggt gca gga gcc gct gct ggc gct gca 1651 Ala Gly Ala Gly Ala Gly Ala Gly Ala Ala Ala Gly Ala Ala 505 510 515 acc gcc gtg gca gct aag ccg aag ctg gcc gct ggg gaa gta gtg gac 1699 Thr Ala Val Ala Ala Lys Pro Lys Leu Ala Ala Gly Glu Val Val Asp 520 525 att gtt tcc cca ctc gaa ggc aag gca att cca ctt tct gaa gta cct 1747 Ile Val Ser Pro Leu Glu Gly Lys Ala Ile Pro Leu Ser Glu Val Pro 535 540 545 gac cca atc ttt gca gca ggc aag ctt gga cca ggc att gca atc caa 1795 Asp Pro Ile Phe Ala Ala Gly Lys Leu Gly Pro Gly Ile Ala Ile Gln 550 555 560 cca act gga aac acc gtt gtt gct cca gca gac gct act gtc atc ctt 1843 Pro Thr Gly Asn Thr Val Val Ala Pro Ala Asp Ala Thr Val Ile Leu 570 575 580 gtc cag aaa tct gga cac gca gtg gca ttg cgc tta gat agc gga gtt Val Gln Lys Ser Gly His Ala Val Ala Leu Arg Leu Asp Ser Gly Val 585 590 gaa atc ctt qtc cac qtt qqa ttq qac acc qtq caa ttq qqc qqc qaa 1939 Glu Ile Leu Val His Val Gly Leu Asp Thr Val Gln Leu Gly Gly Glu 600 605 ggc ttc acc qtt cac qtt qag cgc aqq caq caa gtc aag gcg ggg gat 1987 Gly Phe Thr Val His Val Glu Arg Arg Gln Gln Val Lys Ala Gly Asp 615 620 625

cca ctg atc act ttt gac gct gac ttc att cga tcc aag gat cta cct 2035

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ttg atc acc cca gtt gtg gtg tct aac gcc gcg aaa ttc ggt gaa att 2083

Leu Ile Thr Pro Val Val Val Ser Asn Ala Ala Lys Phe Gly Glu Ile 650 655 660

gaa ggt att cct gca gat cag gca aat tct tcc acg act gtg atc aag 2131

Glu Gly Ile Pro Ala Asp Gln Ala Asn Ser Ser Thr Thr Val Ile Lys
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Arg Phe Gln Val Lys Asp Gln Ser Ile Val Asp Gln Gln Glu Ile Asp 35 40 45

Ser Asp Pro Ser Val Leu Gly Val Val Pro Gln Gly Ser Thr Gly Met 50 60

Gln Val Val Met Gly Gly Ser Val Ala Asn Tyr Tyr Gln Glu Ile Leu 65 70 75 80

Lys Leu Asp Gly Met Lys His Phe Ala Asp Gly Glu Ala Thr Glu Ser 85 90 95

Ser Ser Lys Lys Glu Tyr Gly Gly Val Arg Gly Lys Tyr Ser Trp Ile 100 105 110

Asp Tyr Ala Phe Glu Phe Leu Ser Asp Thr Phe Arg Pro Ile Leu Trp
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Ala Leu Leu Gly Ala Ser Leu Ile Ile Thr Leu Leu Val Leu Ala Asp 130 135 140

Thr Phe Gly Leu Gln Asp Phe Arg Ala Pro Met Asp Glu Gln Pro Asp 145 150 155 160

Thr Tyr Val Phe Leu His Ser Met Trp Arg Ser Val Phe Tyr Phe Leu 165 170 175

Pro Ile Met Val Gly Ala Thr Ala Ala Arg Lys Leu Gly Ala Asn Glu

185

190

180

- 41 -

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Ala Leu Gly Ser Ala Gly Asp Thr Val Thr Val Phe Gly Leu Pro Met

Val Leu Asn Asp Tyr Ser Gly Gln Val Phe Pro Pro Leu Ile Ala Ala 235

Ile Gly Leu Tyr Trp Val Glu Lys Gly Leu Lys Lys Ile Ile Pro Glu

Ala Val Gln Met Val Phe Val Pro Phe Phe Ser Leu Ile Met Ile

Pro Ala Thr Ala Phe Leu Leu Gly Pro Phe Gly Ile Gly Val Gly Asn 280

Gly Ile Ser Asn Leu Leu Glu Ala Ile Asn Asn Phe Ser Pro Phe Ile 295

Leu Ser Ile Val Ile Pro Leu Leu Tyr Pro Phe Leu Val Pro Leu Gly 305 310 315

Leu His Trp Pro Leu Asn Ala Ile Met Ile Gln Asn Ile Asn Thr Leu 330

Gly Tyr Asp Phe Ile Gln Gly Pro Met Gly Ala Trp Asn Phe Ala Cys 340

Phe Gly Leu Val Thr Gly Val Phe Leu Leu Ser Ile Lys Glu Arg Asn 360

Lys Ala Met Arg Gln Val Ser Leu Gly Gly Met Leu Ala Gly Leu Leu

Gly Gly Ile Ser Glu Pro Ser Leu Tyr Gly Val Leu Leu Arg Phe Lys 390

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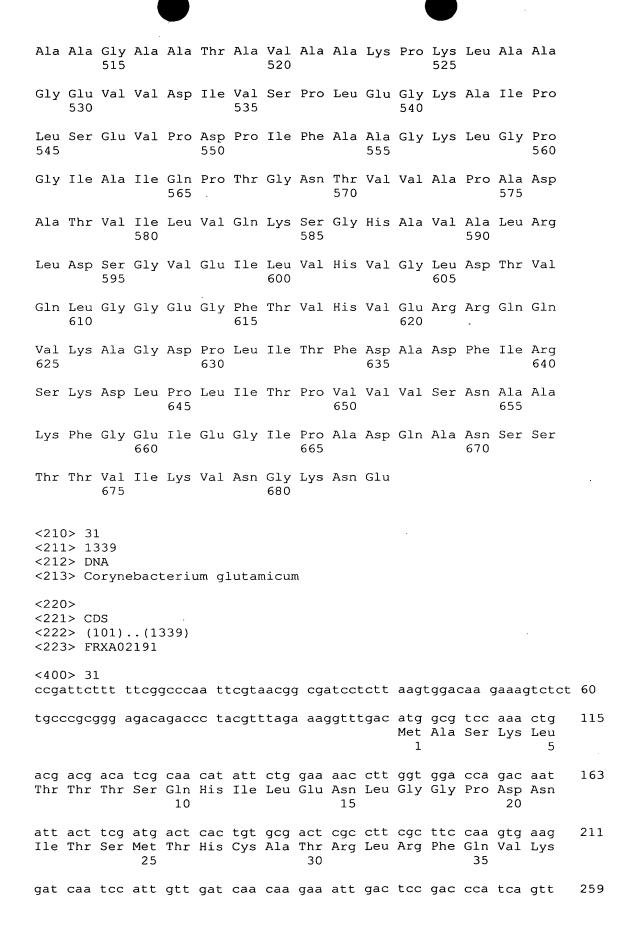
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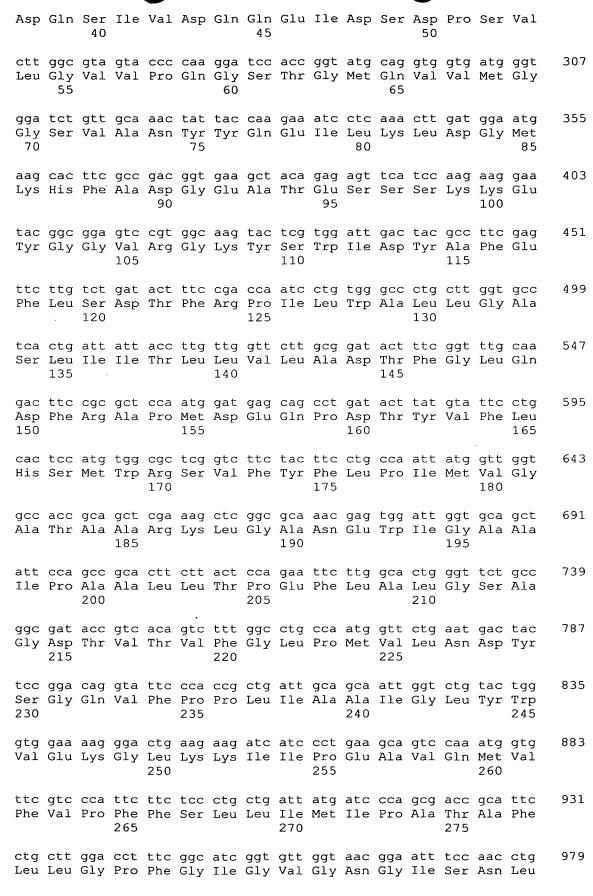
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280

- 44 -

290

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Leu Glu Ala Ile Asn Asn Phe Ser Pro Phe Ile Leu Ser Ile Val Ile 295 cca ttg ctc tac cca ttc ttg gtt cca ctt gga ttg cac tgg cca cta

285

Pro Leu Leu Tyr Pro Phe Leu Val Pro Leu Gly Leu His Trp Pro Leu 310 320 325

aac gcc atc atg atc cag aac atc aac ctg ggt tac gac ttc att 1123

Asn Ala Ile Met Ile Gln Asn Ile Asn Thr Leu Gly Tyr Asp Phe Ile 330 335 340

cag gga cca atg ggt gcc tgg aac ttc gcc tgc ttc ggc ctg gtc acc 1171

Gln Gly Pro Met Gly Ala Trp Asn Phe Ala Cys Phe Gly Leu Val Thr 345 . 350 . 355

ggc gtg ttc ttg ctc tcc att aag gaa cga aac aag gcc atg cgt cag 1219

Gly Val Phe Leu Leu Ser Ile Lys Glu Arg Asn Lys Ala Met Arg Gln 360 365 370

gtt tcc ctg ggt ggc atg ttg gct ggt ttg ctc ggc ggc att tcc gag 1267

Val Ser Leu Gly Gly Met Leu Ala Gly Leu Leu Gly Gly Ile Ser Glu 375 380 385

cct tcc ctc tac ggt gtt ctg ctc cga ttc aag aag acc tac ttc cgc 1315

Pro Ser Leu Tyr Gly Val Leu Leu Arg Phe Lys Lys Thr Tyr Phe Arg 390 395 400 405

ctc ctg ccg ggt tgt ttg gca gca 1339 Leu Leu Pro Gly Cys Leu Ala Ala

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Arg Phe Gln Val Lys Asp Gln Ser Ile Val Asp Gln Gln Glu Ile Asp 35 40 45

Ser Asp Pro Ser Val Leu Gly Val Val Pro Gln Gly Ser Thr Gly Met 50 55 . 60



Gln Val Val Met Gly Gly Ser Val Ala Asn Tyr Tyr Gln Glu Ile Leu 65 70 75 80

Lys Leu Asp Gly Met Lys His Phe Ala Asp Gly Glu Ala Thr Glu Ser 85 90 95

Ser Ser Lys Lys Glu Tyr Gly Gly Val Arg Gly Lys Tyr Ser Trp Ile 100 105 110

Asp Tyr Ala Phe Glu Phe Leu Ser Asp Thr Phe Arg Pro Ile Leu Trp 115 120 125

Ala Leu Leu Gly Ala Ser Leu Ile Ile Thr Leu Leu Val Leu Ala Asp 130 135 140

Thr Phe Gly Leu Gln Asp Phe Arg Ala Pro Met Asp Glu Gln Pro Asp 145 150 155 160

Thr Tyr Val Phe Leu His Ser Met Trp Arg Ser Val Phe Tyr Phe Leu 165 170 175

Pro Ile Met Val Gly Ala Thr Ala Ala Arg Lys Leu Gly Ala Asn Glu 180 185 190

Trp Ile Gly Ala Ala Ile Pro Ala Ala Leu Leu Thr Pro Glu Phe Leu 195 200 205

Ala Leu Gly Ser Ala Gly Asp Thr Val Thr Val Phe Gly Leu Pro Met 210 215 220

Val Leu Asn Asp Tyr Ser Gly Gln Val Phe Pro Pro Leu Ile Ala Ala 225 230 235 240

Ile Gly Leu Tyr Trp Val Glu Lys Gly Leu Lys Lys Ile Ile Pro Glu 245 250 255

Ala Val Gln Met Val Phe Val Pro Phe Phe Ser Leu Leu Ile Met Ile 260 265 270

Pro Ala Thr Ala Phe Leu Leu Gly Pro Phe Gly Ile Gly Val Gly Asn 275 280 285

Gly Ile Ser Asn Leu Leu Glu Ala Ile Asn Asn Phe Ser Pro Phe Ile 290 295 300

Leu Ser Ile Val Ile Pro Leu Leu Tyr Pro Phe Leu Val Pro Leu Gly 305 310 315 320

Leu His Trp Pro Leu Asn Ala Ile Met Ile Gln Asn Ile Asn Thr Leu 325 330 335

Gly Tyr Asp Phe Ile Gln Gly Pro Met Gly Ala Trp Asn Phe Ala Cys 340 345 350

Phe Gly Leu Val Thr Gly Val Phe Leu Leu Ser Ile Lys Glu Arg Asn 355 360 365

Lys Ala Met Arg Gln Val Ser Leu Gly Gly Met Leu Ala Gly Leu Leu 370 375 380

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4



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gtt gaa atc ctt gtc cac gtt gga ttg gac acc gtg caa ttg ggc ggc 192 Val Glu Ile Leu Val His Val Gly Leu Asp Thr Val Gln Leu Gly Gly 50 55 60

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gat cca ctg atc act ttt gac gct gac ttc att cga tcc aag gat cta 288
Asp Pro Leu Ile Thr Phe Asp Ala Asp Phe Ile Arg Ser Lys Asp Leu
85 90 95

cct ttg atc acc cca gtt gtg gtg tct aac gcc gcg aaa ttc ggt gaa 336 Pro Leu Ile Thr Pro Val Val Val Ser Asn Ala Ala Lys Phe Gly Glu 100 105 110

att gaa ggt att cct gca gat cag gca aat tct tcc acg act gtg atc 384
Ile Glu Gly Ile Pro Ala Asp Gln Ala Asn Ser Ser Thr Thr Val Ile
115 120 125

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Val Glu Ile Leu Val His Val Gly Leu Asp Thr Val Gln Leu Gly Gly

Glu Gly Phe Thr Val His Val Glu Arg Arg Gln Gln Val Lys Ala Gly 65 70 75 80

Asp Pro Leu Ile Thr Phe Asp Ala Asp Phe Ile Arg Ser Lys Asp Leu 85 90 95

Pro Leu Ile Thr Pro Val Val Val Ser Asn Ala Ala Lys Phe Gly Glu 100 105 110

Ile Glu Gly Ile Pro Ala Asp Gln Ala Asn Ser Ser Thr Thr Val Ile 115 \$120\$ 125

Lys Val Asn Gly Lys Asn Glu 130 135